

SEQUENCE LISTING

<110> Bryan, Bruce
 Szent-Gyorgyi, Christopher
 Szczepaniak, William

<120> RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
 FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT
 SCREENING AND NOVELTY ITEMS

<130> 24729-128

<140> Not Yet Assigned

<141> Herewith

<150> 60/189,691

<151> 2000-03-15

<150> 09/277,716

<151> 1999-03-26

<150> 08/757,046

<151> 1996-11-25

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<151> 1996-02-06

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<151> 1997-08-08

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<151> 1997-12-12

<160> 33

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<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

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<223> Renilla reniformas luciferase

<400> 1

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| agc tta aag atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg | 48 |
| Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg | |
| 1 5 10 15 | |
| atg ata act ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt | 96 |
| Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val | |
| 20 25 30 | |
| ctt gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat | 144 |
| Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn | |
| 35 40 45 | |
| gct gtt att ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga | 192 |
| Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg | |
| 50 55 60 | |

| | |
|--|------|
| cat gtt gtg cca cat att gag cca gta gcg cgg tgt att ata cca gat | 240 |
| His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp | |
| 65 70 75 80 | |
| ctt att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg | 288 |
| Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg | |
| 85 90 95 | |
| tta ctt gat cat tac aaa tat ctt act gca tgg ttg aac ttc tta att | 336 |
| Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile | |
| 100 105 110 | |
| tac caa aga aga tca ttt ttt gtc ggc cat gat tgg ggt gct tgt ttg | 384 |
| Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu | |
| 115 120 125 | |
| gca ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt | 432 |
| Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val | |
| 130 135 140 | |
| cac gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct | 480 |
| His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro | |
| 145 150 155 160 | |
| gat att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa | 528 |
| Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys | |
| 165 170 175 | |
| atg gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa | 576 |
| Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys | |
| 180 185 190 | |
| atc atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca | 624 |
| Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro | |
| 195 200 205 | |
| ttc aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt | 672 |
| Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg | |
| 210 215 220 | |
| gaa atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt | 720 |
| Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val | |
| 225 230 235 240 | |
| agg aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg | 768 |
| Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met | |
| 245 250 255 | |
| ttt att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc | 816 |
| Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly | |
| 260 265 270 | |
| gcc aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat | 864 |
| Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His | |
| 275 280 285 | |
| ttt tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg | 912 |
| Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser | |
| 290 295 300 | |
| ttc gtt gag cga gtt ctc aaa aat gaa caa taattacttt gggtttttat | 962 |
| Phe Val Glu Arg Val Leu Lys Asn Glu Gln | |
| 305 310 | |
| ttacattttt cccgggttta ataataataaa tgtcattttc aacaatttta ttttaactga | 1022 |

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atatttcaca gggaacattc atatatgttg attaatttag ctggaacttt actctgtcat 1082
atcattttgg aatattacct ctttcaatga aactttataa acagtgggtc aattaattaa 1142
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<212> DNA
<213> Cypridina hilagendorfii luciferase

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<222> (1)...(1665)
<223> Cypridina hilgendorfii luciferase

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aac tgc cag gat gca tgt cct gta gaa gct gaa gca ccg tca agt aca 96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
20 25 30

cca aca gtc cca aca tct tgt gaa gct aaa gaa gga gaa tgt atc gat 144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
35 40 45

acc aga tgc gca aca tgt aaa cga gac ata cta tca gac gga ctg tgt 192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
50 55 60

gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gta att 240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
65 70 75 80

gaa tcc aga gta gaa gct gct gga tat ttt aga acg ttt tac gcc aaa 288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
85 90 95

aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct cga gga acc 336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
100 105 110

aag ggt ggc gac tgg tct gta acc ctc acc atg gag aat cta gat gga 384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
115 120 125

cag aag gga gct gta ctg act aag aca aca ctg gag gta gta gga gac 432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
130 135 140

gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga 480
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145 150 155 160

gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc 528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
165 170 175

att gct gtt gtc gaa ata ccc ggc ttc aat att aca gtc atc gaa ttc 576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
180 185 190

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| | |
|---|------|
| ttt aaa cta atc gtg ata gat att ctg gga gga aga tct gtg aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205 | 624 |
| gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220 | 672 |
| ctg gag atg aat gac gct gat gac ttt act aca gac gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240 | 720 |
| gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tac Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255 | 768 |
| ggg aat cct tct gat atc gaa tac tgc aaa ggt ctc atg gag cca tac Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr 260 265 270 | 816 |
| aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act ctg tcc Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser 275 280 285 | 864 |
| tgc gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val 290 295 300 | 912 |
| ctt ttc gac tat gtt gag aca tgc gct gca ccg gaa acg aga gga acg Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr 305 310 315 320 | 960 |
| tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gcc aga Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg 325 330 335 | 1008 |
| tat caa ttc cag ggc cca tgc aaa gag ctt ctg atg gcc gca gac tgt Tyr Gln Phe Gln Gly Pro Cys Lys Glu Leu Leu Met Ala Ala Asp Cys 340 345 350 | 1056 |
| tac tgg aac aca tgg gat gta aag gtt tca cat aga gat gtt gag tca Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser 355 360 365 | 1104 |
| tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val 370 375 380 | 1152 |
| gat ttg att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val 385 390 395 400 | 1200 |
| tct atc ccg tac agt tct gag aac aca tcc ata tac tgg cag gat gga Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly 405 410 415 | 1248 |
| gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe 420 425 430 | 1296 |
| aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly 435 440 445 | 1344 |
| aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat | 1392 |

| | | | | | | | | | | | | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|-----|-----|-----|-----|-----|----------|------------|-----|-----|------|--|
| Lys | Thr | Cys | Gly | Ile | Cys | Gly | Asn | Tyr | Asn | Gln | Asp | Ser | Thr | Asp | Asp | | |
| 450 | | | | | | 455 | | | | | 460 | | | | | | |
| ttc | ttt | gac | gca | gaa | gga | gca | tgc | gct | ctg | acc | ccc | aat | ccc | cca | gga | 1440 | |
| Phe | Phe | Asp | Ala | Glu | Gly | Ala | Cys | Ala | Leu | Thr | Pro | Asn | Pro | Pro | Gly | | |
| 465 | | | | | 470 | | | | 475 | | | | | | 480 | | |
| tgt | aca | gag | gag | cag | aaa | cca | gaa | gct | gag | cga | ctc | tgc | aat | agt | cta | 1488 | |
| Cys | Thr | Glu | Glu | Gln | Lys | Pro | Glu | Ala | Glu | Arg | Leu | Cys | Asn | Ser | Leu | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| ttt | gat | agt | tct | atc | gac | gag | aaa | tgt | aat | gtc | tgc | tac | aag | cct | gac | 1536 | |
| Phe | Asp | Ser | Ser | Ile | Asp | Glu | Lys | Cys | Asn | Val | Cys | Tyr | Lys | Pro | Asp | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| cgt | att | gca | cga | tgt | atg | tac | gag | tat | tgc | ctg | agg | gga | cag | caa | gga | 1584 | |
| Arg | Ile | Ala | Arg | Cys | Met | Tyr | Glu | Tyr | Cys | Leu | Arg | Gly | Gln | Gln | Gly | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| ttc | tgt | gac | cat | gct | tggt | gag | ttc | aaa | aaa | gaa | tgc | tac | ata | aag | cat | 1632 | |
| Phe | Cys | Asp | His | Ala | Trp | Glu | Phe | Lys | Lys | Glu | Cys | Tyr | Ile | Lys | His | | |
| | 530 | | | | | 535 | | | | | 540 | | | | | | |
| gga | gac | act | cta | gaa | gta | cca | cct | gaa | tgc | caa | taa | aatgaaca | aagatacaga | | | 1685 | |
| Gly | Asp | Thr | Leu | Glu | Val | Pro | Pro | Glu | Cys | Gln | | | | | | | |
| 545 | | | | | 550 | | | | 555 | | | | | | | | |
| agctaagact | actacagcag | aagataaaaag | agaagctgta | gttctttcaaa | aacagtatat | | | | | | | | | | | 1745 | |
| tttgatgtac | tcattgttta | cttacataaa | aataaattgt | tattatcata | acgtaaagaa | | | | | | | | | | | 1805 | |
| aaaaaaaaaa | aaaaaaaa | | | | | | | | | | | | | | | 1822 | |

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 <221> CDS
 <222> (1)...(1644)
 <223> *Luciola cruciata* luciferase
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| atg | gaa | aac | atg | gaa | aac | gat | gaa | aat | att | gta | gtt | gga | cct | aaa | ccg | | 48 |
| Met | Glu | Asn | Met | Glu | Asn | Asp | Glu | Asn | Ile | Val | Val | Gly | Pro | Lys | Pro | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| ttt | tac | cct | atc | gaa | gag | gga | tct | gct | gga | aca | caa | tta | cgc | aaa | tac | | 96 |
| Phe | Tyr | Pro | Ile | Glu | Glu | Gly | Ser | Ala | Gly | Thr | Gln | Leu | Arg | Lys | Tyr | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| atg | gag | cga | tat | gca | aaa | ctt | ggc | gca | att | gct | ttt | aca | aat | gca | gtt | | 144 |
| Met | Glu | Arg | Tyr | Ala | Lys | Leu | Gly | Ala | Ile | Ala | Phe | Thr | Asn | Ala | Val | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| act | ggt | gtt | gat | tat | tct | tac | gcc | gaa | tac | ttg | gag | aaa | tca | tgt | tgt | | 192 |
| Thr | Gly | Val | Asp | Tyr | Ser | Tyr | Ala | Glu | Tyr | Leu | Glu | Lys | Ser | Cys | Cys | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| cta | gga | aaa | gct | ttg | caa | aat | tat | ggt | ttg | gtt | gtt | gat | ggc | aga | att | | 240 |
| Leu | Gly | Lys | Ala | Leu | Gln | Asn | Tyr | Gly | Leu | Val | Val | Asp | Gly | Arg | Ile | | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| gcg | tta | tgc | agt | gaa | aac | tgt | gaa | gaa | ttt | ttt | att | cct | gta | ata | gcc | | 288 |
| Ala | Leu | Cys | Ser | Glu | Asn | Cys | Glu | Glu | Phe | Phe | Ile | Pro | Val | Ile | Ala | | |

| 85 | | | | | | | | | | 90 | | | | | 95 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|
| gga | ctg | ttt | ata | ggt | gta | ggt | gtt | gca | ccc | act | aat | gag | att | tac | act | 336 | | | | |
| Gly | Leu | Phe | Ile | Gly | Val | Gly | Val | Ala | Pro | Thr | Asn | Glu | Ile | Tyr | Thr | | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | | |
| tta | cgt | gaa | ctg | gtt | cac | agt | tta | ggt | atc | tct | aaa | cca | aca | att | gta | 384 | | | | |
| Leu | Arg | Glu | Leu | Val | His | Ser | Leu | Gly | Ile | Ser | Lys | Pro | Thr | Ile | Val | | | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | | | |
| ttt | agt | tct | aaa | aaa | ggc | tta | gat | aaa | gtt | ata | aca | gta | cag | aaa | aca | 432 | | | | |
| Phe | Ser | Ser | Lys | Lys | Gly | Leu | Asp | Lys | Val | Ile | Thr | Val | Gln | Lys | Thr | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | | | |
| gta | act | act | att | aaa | acc | att | gtt | ata | cta | gat | agc | aaa | gtt | gat | tat | 480 | | | | |
| Val | Thr | Thr | Ile | Lys | Thr | Ile | Val | Ile | Leu | Asp | Ser | Lys | Val | Asp | Tyr | | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | | |
| cga | gga | tat | caa | tgt | ctg | gac | acc | ttt | ata | aaa | aga | aac | act | cca | cca | 528 | | | | |
| Arg | Gly | Tyr | Gln | Cys | Leu | Asp | Thr | Phe | Ile | Lys | Arg | Asn | Thr | Pro | Pro | | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | | |
| ggt | ttt | caa | gca | tcc | agt | ttc | aaa | act | gtg | gaa | gtt | gac | cgt | aaa | gaa | 576 | | | | |
| Gly | Phe | Gln | Ala | Ser | Ser | Phe | Lys | Thr | Val | Glu | Val | Asp | Arg | Lys | Glu | | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | | |
| caa | gtt | gct | ctt | ata | atg | aac | tct | tgc | ggt | tct | acc | ggt | ttg | cca | aaa | 624 | | | | |
| Gln | Val | Ala | Leu | Ile | Met | Asn | Ser | Ser | Gly | Ser | Thr | Gly | Leu | Pro | Lys | | | | | |
| | | | 195 | | | | 200 | | | | | 205 | | | | | | | | |
| ggc | gta | caa | ctt | act | cac | gaa | aat | aca | gtc | act | aga | ttt | tct | cat | gct | 672 | | | | |
| Gly | Val | Gln | Leu | Thr | His | Glu | Asn | Thr | Val | Thr | Arg | Phe | Ser | His | Ala | | | | | |
| | | | 210 | | | 215 | | | | | 220 | | | | | | | | | |
| aga | gat | ccg | att | tat | ggt | aac | caa | gtt | tca | cca | ggc | acc | gct | gtt | tta | 720 | | | | |
| Arg | Asp | Pro | Ile | Tyr | Gly | Asn | Gln | Val | Ser | Pro | Gly | Thr | Ala | Val | Leu | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | | |
| act | gtc | gtt | cca | ttc | cat | cat | ggt | ttt | ggt | atg | ttc | act | act | cta | ggg | 768 | | | | |
| Thr | Val | Val | Pro | Phe | His | His | Gly | Phe | Gly | Met | Phe | Thr | Thr | Leu | Gly | | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | | |
| tat | tta | att | tgt | ggt | ttt | cgt | gtt | gta | atg | tta | aca | aaa | ttc | gat | gaa | 816 | | | | |
| Tyr | Leu | Ile | Cys | Gly | Phe | Arg | Val | Val | Met | Leu | Thr | Lys | Phe | Asp | Glu | | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | | |
| gaa | aca | ttt | tta | aaa | act | cta | caa | gat | tat | aaa | tgt | aca | agt | gtt | att | 864 | | | | |
| Glu | Thr | Phe | Leu | Lys | Thr | Leu | Gln | Asp | Tyr | Lys | Cys | Thr | Ser | Val | Ile | | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | | |
| ctt | gta | ccg | acc | ttg | ttt | gca | att | ctc | aac | aaa | agt | gaa | tta | ctc | aat | 912 | | | | |
| Leu | Val | Pro | Thr | Leu | Phe | Ala | Ile | Leu | Asn | Lys | Ser | Glu | Leu | Leu | Asn | | | | | |
| | | | 290 | | | 295 | | | | | 300 | | | | | | | | | |
| aaa | tac | gat | ttg | tca | aat | tta | gtt | gag | att | gca | tct | ggc | gga | gca | cct | 960 | | | | |
| Lys | Tyr | Asp | Leu | Ser | Asn | Leu | Val | Glu | Ile | Ala | Ser | Gly | Gly | Ala | Pro | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | |
| tta | tca | aaa | gaa | gtt | ggt | gaa | gct | gtt | gct | aga | cgc | ttt | aat | ctt | ccc | 1008 | | | | |
| Leu | Ser | Lys | Glu | Val | Gly | Glu | Ala | Val | Ala | Arg | Arg | Phe | Asn | Leu | Pro | | | | | |
| | | | | 325 | | | | 330 | | | | | | 335 | | | | | | |
| ggt | gtt | cgt | caa | ggt | tat | ggt | tta | aca | gaa | aca | aca | tct | gcc | att | att | 1056 | | | | |
| Gly | Val | Arg | Gln | Gly | Tyr | Gly | Leu | Thr | Glu | Thr | Thr | Ser | Ala | Ile | Ile | | | | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | | | | |

att aca cca gaa gga gac gat aaa cca gga gct tct gga aaa gtc gtg 1104
 Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
 355 360 365
 ccg ttg ttt aaa gca aaa gtt att gat ctt gat acc aaa aaa tct tta 1152
 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Ser Leu
 370 375 380
 ggt cct aac aga cgt gga gaa gtt tgt gtt aaa gga cct atg ctt atg 1200
 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
 385 390 395 400
 aaa ggt tat gta aat aat cca gaa gca aca aaa gaa ctt att gac gaa 1248
 Lys Gly Tyr Val Asn Asn Pro Glu Ala Thr Lys Glu Leu Ile Asp Glu
 405 410 415
 gaa ggt tgg ctg cac acc gga gat att gga tat tat gat gaa gaa aaa 1296
 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
 420 425 430
 cat ttc ttt att gtc gat cgt ttg aag tct tta atc aaa tac aaa gga 1344
 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
 435 440 445
 tac caa gta cca cct gcc gaa tta gaa tcc gtt ctt ttg caa cat cca 1392
 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
 450 455 460
 tct atc ttt gat gct ggt gtt gcc ggc gtt cct gat cct gta gct ggc 1440
 Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly
 465 470 475 480
 gag ctt cca gga gcc gtt gtt gta ctg gaa agc gga aaa aat atg acc 1488
 Glu Leu Pro Gly Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr
 485 490 495
 gaa aaa gaa gta atg gat tat gtt gca agt caa gtt tca aat gca aaa 1536
 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
 500 505 510
 cgt tta cgt ggt ggt gtt cgt ttt gtg gat gaa gta cct aaa ggt ctt 1584
 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
 515 520 525
 act gga aaa att gac ggc aga gca att aga gaa atc ctt aag aaa cca 1632
 Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro
 530 535 540
 gtt gct aag atg 1644
 Val Ala Lys Met
 545

<210> 4
 <211> 1820
 <212> DNA
 <213> Vargula (cypridina)
 <220>
 <221> CDS
 <222> (1)...(1665)
 <223> Vargula (cypridina) luciferase
 <400> 4

| | |
|---|-----|
| atg aag ata ata att ctg tct gtt ata ttg gcc tac tgt gtc acc gac Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp 1 5 10 15 | 48 |
| aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr 20 25 30 | 96 |
| cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp 35 40 45 | 144 |
| acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys 50 55 60 | 192 |
| gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile 65 70 75 80 | 240 |
| gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys 85 90 95 | 288 |
| aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr 100 105 110 | 336 |
| aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga Lys Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly 115 120 125 | 384 |
| cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp 130 135 140 | 432 |
| gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly 145 150 155 160 | 480 |
| gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr 165 170 175 | 528 |
| att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe 180 185 190 | 576 |
| ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtc aga att Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205 | 624 |
| gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220 | 672 |
| ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240 | 720 |
| gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255 | 768 |
| ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac | 816 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Gly | Asn | Pro | Ser | Asp | Ile | Glu | Tyr | Cys | Lys | Gly | Leu | Met | Glu | Pro | Tyr | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| aga | gct | gta | tgt | cgt | aac | aat | atc | aac | ttc | tac | tat | tac | act | cta | tcc | 864 |
| Arg | Ala | Val | Cys | Arg | Asn | Asn | Ile | Asn | Phe | Tyr | Tyr | Tyr | Thr | Leu | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| tgt | gcc | ttc | gct | tac | tgt | atg | gga | gga | gaa | gaa | aga | gct | aaa | cac | gtc | 912 |
| Cys | Ala | Phe | Ala | Tyr | Cys | Met | Gly | Gly | Glu | Glu | Arg | Ala | Lys | His | Val | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| ctt | ttc | gac | tat | gtt | gag | aca | tgc | gct | gcg | ccg | gaa | acg | aga | gga | acg | 960 |
| Leu | Phe | Asp | Tyr | Val | Glu | Thr | Cys | Ala | Ala | Pro | Glu | Thr | Arg | Gly | Thr | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| tgt | gtt | tta | tca | gga | cat | act | ttc | tat | gac | aca | ttc | gac | aaa | gca | aga | 1008 |
| Cys | Val | Leu | Ser | Gly | His | Thr | Phe | Tyr | Asp | Thr | Phe | Asp | Lys | Ala | Arg | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| tat | caa | ttc | cag | ggc | cca | tgc | aag | gag | att | ctg | atg | gcc | gca | gac | tgt | 1056 |
| Tyr | Gln | Phe | Gln | Gly | Pro | Cys | Lys | Glu | Ile | Leu | Met | Ala | Ala | Asp | Cys | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| tac | tgg | aac | aca | tgg | gat | gta | aag | gtt | tca | cat | aga | gac | gtc | gaa | tca | 1104 |
| Tyr | Trp | Asn | Thr | Trp | Asp | Val | Lys | Val | Ser | His | Arg | Asp | Val | Glu | Ser | |
| | | 355 | | | | 360 | | | | | | 365 | | | | |
| tac | act | gag | gta | gag | aaa | gta | aca | atc | agg | aaa | cag | tca | act | gta | gta | 1152 |
| Tyr | Thr | Glu | Val | Glu | Lys | Val | Thr | Ile | Arg | Lys | Gln | Ser | Thr | Val | Val | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| gat | ctc | att | gtg | gat | ggc | aag | cag | gtc | aag | gtt | gga | gga | gtg | gat | gta | 1200 |
| Asp | Leu | Ile | Val | Asp | Gly | Lys | Gln | Val | Lys | Val | Gly | Gly | Val | Asp | Val | |
| 385 | | | | | 390 | | | | 395 | | | | | | 400 | |
| tct | atc | ccg | tac | agc | tct | gag | aac | act | tcc | ata | tac | tgg | cag | gat | gga | 1248 |
| Ser | Ile | Pro | Tyr | Ser | Ser | Glu | Asn | Thr | Ser | Ile | Tyr | Trp | Gln | Asp | Gly | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| gac | atc | ctg | acg | acg | gcc | atc | cta | cct | gaa | gct | ctt | gtc | gtt | aag | ttc | 1296 |
| Asp | Ile | Leu | Thr | Thr | Ala | Ile | Leu | Pro | Glu | Ala | Leu | Val | Val | Lys | Phe | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| aac | ttt | aag | cag | ctc | ctt | gta | gtt | cat | atc | aga | gat | cca | ttc | gat | gca | 1344 |
| Asn | Phe | Lys | Gln | Leu | Leu | Val | Val | His | Ile | Arg | Asp | Pro | Phe | Asp | Ala | |
| | | 435 | | | | 440 | | | | | | 445 | | | | |
| aag | aca | tgc | ggc | ata | tgt | ggt | aac | tat | aat | caa | gat | tca | act | gat | gat | 1392 |
| Lys | Thr | Cys | Gly | Ile | Cys | Gly | Asn | Tyr | Asn | Gln | Asp | Ser | Thr | Asp | Asp | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| ttc | ttt | gac | gca | gaa | gga | gca | tgc | gct | cta | acc | ccc | aac | ccc | cca | gga | 1440 |
| Phe | Phe | Asp | Ala | Glu | Gly | Ala | Cys | Ala | Leu | Thr | Pro | Asn | Pro | Pro | Gly | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| tgt | aca | gag | gaa | cag | aaa | cca | gaa | gct | gag | cga | ctt | tgc | aat | aat | ctc | 1488 |
| Cys | Thr | Glu | Glu | Gln | Lys | Pro | Glu | Ala | Glu | Arg | Leu | Cys | Asn | Asn | Leu | |
| | | | | 485 | | | | 490 | | | | | | 495 | | |
| ttt | gat | tct | tct | atc | gac | gag | aaa | tgt | aat | gtc | tgc | tac | aag | cct | gac | 1536 |
| Phe | Asp | Ser | Ser | Ile | Asp | Glu | Lys | Cys | Asn | Val | Cys | Tyr | Lys | Pro | Asp | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| cgg | att | gcc | cga | tgt | atg | tac | gag | tat | tgc | ctg | agg | gga | caa | caa | gga | 1584 |
| Arg | Ile | Ala | Arg | Cys | Met | Tyr | Glu | Tyr | Cys | Leu | Arg | Gly | Gln | Gln | Gly | |

| 515 | 520 | 525 | |
|--------------------------------|------------------------|------------------------|------|
| ttt tgt gac cat gct tgg | gag ttc aag aaa gaa | tgc tac ata aaa cat | 1632 |
| Phe Cys Asp His Ala Trp | Glu Phe Lys Lys Glu | Cys Tyr Ile Lys His | |
| 530 | 535 | 540 | |
| gga gac act cta gaa gta | cca cct gaa tgt caa | taaacgtaca aagatacaga | 1685 |
| Gly Asp Thr Leu Glu Val | Pro Pro Glu Cys Gln | | |
| 545 | 550 | 555 | |
| agctaaggct actacagcag | aagataaaaa agaaactgta | gttccttcaa aaaccgtgta | 1745 |
| ttttatgtac tcattgttta | attagagcaa aataaattgt | tattatcata acttaaaacta | 1805 |
| aaaaaaaaaaaa aaaaa | | | 1820 |
| <210> 5 | | | |
| <211> 958 | | | |
| <212> DNA | | | |
| <213> Aequorea victoria | | | |
| <220> | | | |
| <221> CDS | | | |
| <222> (115)...(702) | | | |
| <223> Apoequorin-encoding gene | | | |
| <400> 5 | | | |
| ggggggggggg ggggggggggg | ggggggggggg gggaatgcaa | ttcatctttg catcaaagaa | 60 |
| ttacatcaaaa tctctagtgtg | atcaactaaa ttgtctcgac | aacaacaagc aaac atg | 117 |
| | | Met | |
| | | 1 | |
| aca agc aaa caa tac tca | gtc aag ctt aca tca | gac ttc gac aac cca | 165 |
| Thr Ser Lys Gln Tyr Ser | Val Lys Leu Thr Ser | Asp Phe Asp Asn Pro | |
| 5 | 10 | 15 | |
| aga tgg att gga cga cac | aag cat atg ttc aat | ttc ctt gat gtc aac | 213 |
| Arg Trp Ile Gly Arg His | Lys His Met Phe Asn | Phe Leu Asp Val Asn | |
| 20 | 25 | 30 | |
| cac aat gga aaa atc tct | ctt gac gag atg gtc | tac aag gca tct gat | 261 |
| His Asn Gly Lys Ile Ser | Leu Asp Glu Met Val | Tyr Lys Ala Ser Asp | |
| 35 | 40 | 45 | |
| att gtc atc aat aac ctt | gga gca aca cct gag | caa gcc aaa cga cac | 309 |
| Ile Val Ile Asn Asn Leu | Gly Ala Thr Pro Glu | Gln Ala Lys Arg His | |
| 50 | 55 | 60 | |
| aaa gat gct gta gaa gcc | ttc ttc gga gga gct | gga atg aaa tat ggt | 357 |
| Lys Asp Ala Val Glu Ala | Phe Phe Gly Gly Ala | Gly Met Lys Tyr Gly | |
| 70 | 75 | 80 | |
| gtg gaa act gat tgg cct | gca tat att gaa gga | tgg aaa aaa ttg gct | 405 |
| Val Glu Thr Asp Trp Pro | Ala Tyr Ile Glu Gly | Trp Lys Lys Leu Ala | |
| 85 | 90 | 95 | |
| act gat gaa ttg gag aaa | tac gcc aaa aac gaa | cca acg ctc atc cgt | 453 |
| Thr Asp Glu Leu Glu Lys | Tyr Ala Lys Asn Glu | Pro Thr Leu Ile Arg | |
| 100 | 105 | 110 | |
| ata tgg ggt gat gct ttg | ttt gat atc gtt gac | aaa gat caa aat gga | 501 |
| Ile Trp Gly Asp Ala Leu | Phe Asp Ile Val Asp | Lys Asp Gln Asn Gly | |
| 115 | 120 | 125 | |
| gcc att aca ctg gat gaa | tgg aaa gca tac acc | aaa gct gct ggt atc | 549 |
| Ala Ile Thr Leu Asp Glu | Trp Lys Ala Tyr Thr | Lys Ala Ala Gly Ile | |
| 130 | 135 | 140 | |
| | | 145 | |

atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat att 597
 Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile
 150 155 160

gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat tta 645
 Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
 165 170 175

gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt gga 693
 Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly
 180 185 190

gct gtc ccc taagaagctc tacgggtggtg atgcacccta ggaagatgat 742
 Ala Val Pro
 195

gtgattttga ataaaacact gatgaattca atcaaaat tccaaat tgaacgattt 802
 caatcggttg tggtgatttt tgtaattagg aacagattaa atcgaatgat tagttgtttt 862
 tttaatcaac agaacttaca aatcgaaaaa gtataaaaaa aaaaaaaaaa aaaaaaaaaa 922
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 958

<210> 6
 <211> 591
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (1)...(588)
 <223> Recombinant Aequorin AEQ1

<400> 6
 atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat 240
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att gac aaa gac caa aat 384
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn
 115 120 125

| | |
|---|-----|
| gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gat ggc | 432 |
| Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly | |
| 130 135 140 | |
| | |
| atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat | 480 |
| Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp | |
| 145 150 155 160 | |
| | |
| att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat | 528 |
| Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His | |
| 165 170 175 | |
| | |
| tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt | 576 |
| Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly | |
| 180 185 190 | |
| | |
| gga gct gtc ccc taa | 591 |
| Gly Ala Val Pro | |
| 195 | |

<210> 7
 <211> 591
 <212> DNA
 <213> Aequoria victoria

 <220>
 <221> CDS
 <222> (1)...(588)
 <223> Recombinant Aequorin AEQ2

| | |
|---|-----|
| <400> 7 | |
| atg acc agc gaa caa tac tca gtc aag ctt aca tca gac ttc gac aac | 48 |
| Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asn Asn | |
| 1 5 10 15 | |
| | |
| cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc | 96 |
| Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val | |
| 20 25 30 | |
| | |
| aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct | 144 |
| Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser | |
| 35 40 45 | |
| | |
| gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga | 192 |
| Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg | |
| 50 55 60 | |
| | |
| cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gga atg aaa tat | 240 |
| His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr | |
| 65 70 75 80 | |
| | |
| ggt gtg gaa act gat tgg cct gca tat att gaa gga tgg aaa aaa ttg | 288 |
| Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu | |
| 85 90 95 | |
| | |
| gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc | 336 |
| Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile | |
| 100 105 110 | |
| | |
| cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat | 384 |
| Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn | |
| 115 120 125 | |

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt 432
 Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
 130 135 140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa agt gga caa ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc taa 591
 Gly Ala Val Pro
 195

<210> 8

<211> 591

<212> DNA

<213> Aequoria victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Recombinant Aequorin AEQ3

<400> 8

atg acc agc gaa caa tac tca gtc aag ctt aca tca gac ttc gac aac 48
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
 1 5 10 15

cca aga tgg att gga cga cac aag cat atg ttc aat ttc ctt gat gtc 96
 Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 20 25 30

aac cac aat gga aaa atc tct ctt gac gag atg gtc tac aag gca tct 144
 Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 35 40 45

gat att gtc atc aat aac ctt gga gca aca cct gag caa gcc aaa cga 192
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 50 55 60

cac aaa gat gct gta gga gac ttc ttc gga gga gct gga atg aaa tat 240
 His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr
 65 70 75 80

ggt gtg gaa act gat tgg cct gca tac att gaa gga tgg aaa aaa ttg 288
 Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
 85 90 95

gct act gat gaa ttg gag aaa tac gcc aaa aac gaa cca acg ctc atc 336
 Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
 100 105 110

cgt ata tgg ggt gat gct ttg ttc gat atc gtt gac aaa gat caa aat 384
 Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
 115 120 125

gga gcc att aca ctg gat gaa tgg aaa gca tac acc aaa gct gct ggt 432

Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
 130 135 140

atc atc caa tca tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa aat gga caa ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc taa 591
 Gly Ala Val Pro
 195

<210> 9
 <211> 567
 <212> DNA
 <213> Aequoria victoria

<220>
 <221> CDS
 <222> (1)...(567)
 <223> Aequorin photoprotein

<400> 9

gtc aag ctt aca cca gac ttc gac aac cca aaa tgg att gga cga cac 48
 Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1 5 10 15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct 96
 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
 20 25 30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt 144
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
 35 40 45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc 192
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
 50 55 60

ttc ttc gga gga gct gca atg aaa tat ggt gta gaa act gaa tgg cct 240
 Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
 65 70 75 80

gaa tac atc gaa gga tgg aaa aga ctg gct tcc gag gaa ttg aaa agg 288
 Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg
 85 90 95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg 336
 Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
 100 105 110

ttc gat atc att gac aaa gac caa aat gga gct att tca ctg gat gaa 384
 Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu
 115 120 125

tgg aaa gca tac acc aaa tct gct ggc atc atc caa tcg tca gaa gat 432
 Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp
 130 135 140

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc 480
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
 145 150 155 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg 528
 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
 165 170 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc 567
 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
 180 185

<210> 10

<211> 588

<212> DNA

<213> Aequoria victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Aequorin mutant w/increased bioluminescence
 activity

<400> 10

atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
 115 120 125

gga gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc 432
 Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
 130 135 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc 588
 Gly Ala Val Pro
 195

<210> 11

<211> 588

<212> DNA

<213> Aequarea victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Recombinant site-directed Aequarein mutant

<400> 11

atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
 115 120 125

gga gct att tca ctg gat tca tgg aaa gca tac acc aaa tct gct ggc 432
 Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly
 130 135 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc 588
 Gly Ala Val Pro
 195

<210> 12

<211> 588

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (1)...(588)

<223> Aequorin mutant with increased bioluminescence activity

<400> 12

atg acc agc gaa caa tac tca gtc aag ctt aca cca gac ttc gac aac 48
 Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1 5 10 15

cca aaa tgg att gga cga cac aag cac atg ttt aat ttt ctt gat gtc 96
 Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 20 25 30

aac cac aat gga agg atc tct ctt gac gag atg gtc tac aag gcg tcc 144
 Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 35 40 45

gat att gtt ata aac aat ctt gga gca aca cct gaa caa gcc aaa cgt 192
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 50 55 60

cac aaa gat gct gta gaa gcc ttc ttc gga gga gct gca atg aaa tat 240
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
 65 70 75 80

ggt gta gaa act gaa tgg cct gaa tac atc gaa gga tgg aaa aga ctg 288
 Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
 85 90 95

gct tcc gag gaa ttg aaa agg tat tca aaa aac caa atc aca ctt att 336
 Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
 100 105 110

cgt tta tgg ggt gat gca ttg ttc gat atc att tcc aaa gac caa aat 384
 Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
 115 120 125

gca gct att tca ctg gat gaa tgg aaa gca tac acc aaa tct gct ggc 432
 Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
 130 135 140

atc atc caa tcg tca gaa gat tgc gag gaa aca ttc aga gtg tgc gat 480
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 145 150 155 160

att gat gaa agt gga cag ctc gat gtt gat gag atg aca aga caa cat 528
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
 165 170 175

tta gga ttt tgg tac acc atg gat cct gct tgc gaa aag ctc tac ggt 576
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
 180 185 190

gga gct gtc ccc 588
 Gly Ala Val Pro
 195

<210> 13
 <211> 567
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (1)...(567)
 <223> Recombinant apoaequorin (AQUALITEp)

<400> 13
 gtc aag ctt aca cca gac ttc gac aac cca aaa tgg att gga cga cac 48
 Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1 5 10 15

aag cac atg ttt aat ttt ctt gat gtc aac cac aat gga agg atc tct 96
 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
 20 25 30

ctt gac gag atg gtc tac aag gcg tcc gat att gtt ata aac aat ctt 144
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
 35 40 45

gga gca aca cct gaa caa gcc aaa cgt cac aaa gat gct gta gaa gcc 192
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
 50 55 60

ttc ttc gga gga gct gga atg aaa tat ggt gta gaa act gaa tgg cct 240
 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
 65 70 75 80

gaa tac atc gaa gga tgg aaa aaa ctg gct tcc gag gaa ttg aaa agg 288
 Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg
 85 90 95

tat tca aaa aac caa atc aca ctt att cgt tta tgg ggt gat gca ttg 336
 Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
 100 105 110

ttc gat atc att gac aaa gac caa aat gga gct att ctg tca gat gaa 384
 Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu
 115 120 125

tgg aaa gca tac acc aaa tct gat ggc atc atc caa tcg tca gaa gat 432
 Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Lys Ser Ser Glu Asp
 130 135 140

tgc gag gaa aca ttc aga gtg tgc gat att gat gaa agt gga cag ctc 480
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
 145 150 155 160

gat gtt gat gag atg aca aga caa cat tta gga ttt tgg tac acc atg 528

Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
 165 170 175

gat cct gct tgc gaa aag ctc tac ggt gga gct gtc ccc
 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
 180 185

567

<210> 14
 <211> 236
 <212> PRT
 <213> *Vibrio fisheri*

<400> 14
 Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn
 1 5 10 15
 Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
 20 25 30
 Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
 35 40 45
 Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
 50 55 60
 Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
 65 70 75 80
 Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
 85 90 95
 His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
 100 105 110
 Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
 115 120 125
 Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
 130 135 140
 Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
 145 150 155 160
 Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
 165 170 175
 Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp
 180 185 190
 Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
 195 200 205
 Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
 210 215 220
 Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
 225 230 235

<210> 15
 <211> 1079
 <212> DNA
 <213> *Renilla mulleri*

<220>
 <221> CDS
 <222> (259)...(975)
 <223> *Renilla mulleri* GFP

<400> 15
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 gtattttacgt cagacctgtc taatcgaaac cacaacaaac tcttaaaata agccacattt 120
 acataatatc taagagacgc ctcatTTaag agtagtaaaa atataatata tgatagagta 180
 tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttgTTaa tgcaatcgaa 240
 agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta 291
 Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
 1 5 10

caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac 339
 Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
 15 20 25

cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc 387
 His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
 30 35 40

aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt 435
 Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
 45 50 55

gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc 483
 Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe
 60 65 70 75

acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca 531
 Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
 80 85 90

gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt 579
 Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
 95 100 105

gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac 627
 Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
 110 115 120

aga gtg gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg 675
 Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met
 125 130 135

cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg 723
 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
 140 145 150 155

aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac 771
 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
 160 165 170

tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa 819
 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
 175 180 185

ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg 867
 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
 190 195 200

gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act 915
 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
 205 210 215

gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac 963
 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
 220 225 230 235

gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca 1015
 Glu Trp Val *

aataataatt ttttaaacaa ttatcaatgt tttgtgatat gtttgtaaaaa aaaaaaaaaa 1075
 aaaa 1079

<210> 16
 <211> 238

<212> PRT

<213> Renilla mulleri

<400> 16

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Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
 1      5      10      15
Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
      20      25      30
Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
      35      40      45
Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
      50      55      60
Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
      65      70      75      80
Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
      85      90      95
Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
      100      105      110
Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
      115      120      125
Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
      130      135      140
Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
      145      150      155      160
Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
      165      170      175
Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
      180      185      190
Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
      195      200      205
Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
      210      215      220
Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
      225      230      235

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<210> 17

<211> 1217

<212> DNA

<213> Renilla mulleri

<220>

<221> CDS

<222> (31)...(963)

<223> Renilla mulleri luciferase

<400> 17

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cggcacgagg ttttaagaatc aataaaaaaaaa atg acg tca aaa gtt tac gat cct      54
                      Met Thr Ser Lys Val Tyr Asp Pro
                        1                      5

gaa tta aga aaa cgc atg att act ggt cca caa tgg tgg gca aga tgt      102
Glu Leu Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys
      10      15      20

aaa caa atg aat gtt ctt gat tca ttt att aat tat tat gat tca gaa      150
Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu
      25      30      35      40

aaa cat gca gaa aat gca gtt ata ttt tta cat ggt aat gca gca tct      198
Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser
                        45      50      55

tct tat tta tgg cgt cat gtt gta cca cat gtt gaa cca gtg gcg cga      246
Ser Tyr Leu Trp Arg His Val Val Pro His Val Glu Pro Val Ala Arg
                        60      65      70

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| | |
|---|------|
| tgt att ata cca gat ctt ata ggt atg ggt aaa tca ggc aag tct ggt | 294 |
| Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly | |
| 75 80 85 | |
| aat ggt tcc tat aga tta cta gat cat tac aaa tat ctt act gaa tgg | 342 |
| Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Glu Trp | |
| 90 95 100 | |
| ttc aaa cat ctt aat tta cca aag aag atc att ttt gtc ggt cat gat | 390 |
| Phe Lys His Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp | |
| 105 110 115 120 | |
| tgg ggt gct tgt tta gca ttt cat tat tgc tat gaa cat cag gat cgc | 438 |
| Trp Gly Ala Cys Leu Ala Phe His Tyr Cys Tyr Glu His Gln Asp Arg | |
| 125 130 135 | |
| atc aaa gca gtt gtt cat gct gaa agt gta gta gat gtg att gaa tcg | 486 |
| Ile Lys Ala Val Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser | |
| 140 145 150 | |
| tgg gac gaa tgg cct gat att gaa gaa gat att gct ttg att aaa tct | 534 |
| Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser | |
| 155 160 165 | |
| gaa gaa gga gaa aaa atg gtt tta gag aat aac ttc ttc gtg gaa acc | 582 |
| Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr | |
| 170 175 180 | |
| atg ttg cca tca aaa atc atg aga aag ttg gaa cca gag gaa ttt gct | 630 |
| Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala | |
| 185 190 195 200 | |
| gct tat ctt gaa cca ttt aaa gag aaa ggt gaa gtt cgt cgt cca aca | 678 |
| Ala Tyr Leu Glu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr | |
| 205 210 215 | |
| tta tca tgg cct cgt gaa atc cct ttg gta aaa ggt ggt aaa ccg gat | 726 |
| Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp | |
| 220 225 230 | |
| gta gta gaa att gtc agg aat tat aat gct tat ctt cgt gca agt cat | 774 |
| Val Val Glu Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser His | |
| 235 240 245 | |
| gat tta cca aaa atg ttt att gaa tct gat cca gga ttc ttt tcc aat | 822 |
| Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn | |
| 250 255 260 | |
| gct att gtt gaa ggt gct aag aaa ttc cct aat act gaa ttt gtt aaa | 870 |
| Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys | |
| 265 270 275 280 | |
| gtc aaa ggt ctt cat ttt tca caa gaa gat gca cct gat gaa atg gga | 918 |
| Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly | |
| 285 290 295 | |
| aat tat ata aaa tcg ttt gtt gag cgt gtt ctt aaa aat gaa caa | 963 |
| Asn Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln | |
| 300 305 310 | |
| taaactacca gggtttccatg ttgccacttt agctggggttt aataaatttc actatcaatt | 1023 |
| tgaacaattt cacattaatt ttaactatta aaaaattatg gacacagggg ttatatcaga | 1083 |
| tgattaattt agttgggaac aatgaatacc gaataattatg aattctcttt agctatttat | 1143 |
| aataatcaca ttcttatgta ataaaacttt gttttaataa attaattgatt cagaaaaaaa | 1203 |

aaaaaaaaaa aaaa

1217

<210> 18
 <211> 311
 <212> PRT
 <213> Renilla mulleri

<400> 18
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 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
 20 25 30
 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
 35 40 45
 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
 50 55 60
 Pro His Val Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65 70 75 80
 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
 85 90 95
 His Tyr Lys Tyr Leu Thr Glu Trp Phe Lys His Leu Asn Leu Pro Lys
 100 105 110
 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
 115 120 125
 Tyr Cys Tyr Glu His Gln Asp Arg Ile Lys Ala Val His Ala Glu
 130 135 140
 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
 145 150 155 160
 Glu Asp Ile Ala Leu Ile Lys Ser Glu Gly Glu Lys Met Val Leu
 165 170 175
 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
 180 185 190
 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
 195 200 205
 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
 210 215 220
 Leu Val Lys Gly Gly Lys Pro Asp Val Val Glu Ile Val Arg Asn Tyr
 225 230 235 240
 Asn Ala Tyr Leu Arg Ala Ser His Asp Leu Pro Lys Met Phe Ile Glu
 245 250 255
 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
 260 265 270
 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
 275 280 285
 Glu Asp Ala Pro Asp Glu Met Gly Asn Tyr Ile Lys Ser Phe Val Glu
 290 295 300
 Arg Val Leu Lys Asn Glu Gln
 305 310

<210> 19
 <211> 765
 <212> DNA
 <213> Gaussia

<220>
 <221> CDS
 <222> (37)...(594)

<400> 19
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 Met Gly Val Lys Val Leu
 1 5

ttt gcc ctt att tgt att gct gtg gcc gag gcc aaa cca act gaa aac 102
 Phe Ala Leu Ile Cys Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn

| 10 | 15 | 20 | |
|---|----|----|-----|
| aat gaa gat ttc aac att gta gct gta gct agc aac ttt gct aca acg | | | 150 |
| Asn Glu Asp 25 Phe Asn Ile Val 30 Ala Val Ala Ser Asn Phe Ala Thr Thr | | | |
| gat ctc gat gct gac cgt ggt aaa ttg ccc gga aaa aaa tta cca ctt | | | 198 |
| Asp Leu 40 Asp Ala Asp Arg Gly 45 Lys Leu Pro Gly Lys 50 Lys Leu Pro Leu | | | |
| gag gta ctc aaa gaa atg gaa gcc aat gct agg aaa gct ggc tgc act | | | 246 |
| Glu Val Leu Lys Glu Met 60 Glu Ala Asn Ala Arg 65 Lys Ala Gly Cys Thr 70 | | | |
| agg gga tgt ctg ata tgc ctg tca cac atc aag tgt aca ccc aaa atg | | | 294 |
| Arg Gly Cys Leu Ile 75 Cys Leu Ser His Ile 80 Lys Cys Thr Pro Lys Met 85 | | | |
| aag aag ttt atc cca gga aga tgc cac acc tat gaa gga gac aaa gaa | | | 342 |
| Lys Lys Phe 90 Ile Pro Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu 100 | | | |
| agt gca cag gga gga ata gga gag gct att gtt gac att cct gaa att | | | 390 |
| Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile 105 110 115 | | | |
| cct ggg ttt aag gat ttg gaa ccc atg gaa caa ttc att gca caa gtt | | | 438 |
| Pro Gly Phe Lys Asp Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val 120 125 130 | | | |
| gac cta tgt gta gac tgc aca act gga tgc ctc aaa ggt ctt gcc aat | | | 486 |
| Asp Leu Cys Val Asp Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn 135 140 145 150 | | | |
| gtg caa tgt tct gat tta ctc aag aaa tgg ctg cca caa aga tgt gca | | | 534 |
| Val Gln Cys Ser Asp 155 Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala 160 165 | | | |
| act ttt gct agc aaa att caa ggc caa gtg gac aaa ata aag ggt gcc | | | 582 |
| Thr Phe Ala Ser Lys Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala 170 175 180 | | | |
| ggg ggt gat taa tcctaataaga atactgcata actggatgat gatatactag | | | 634 |
| Gly Gly Asp 185 * | | | |
| cttattgctc ataaaaatggc catttttttgt aacaaatcga gtctatgtaa ttcaaaatac | | | 694 |
| ctaattaatt gttaatacat atgtaattcc tataaatata atttatgcaa tccaaaaaaa | | | 754 |
| aaaaaaaaa a | | | 765 |

<210> 20
 <211> 185
 <212> PRT
 <213> Renilla mulleri

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 Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
 1 5 10 15
 Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
 20 25 30
 Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
 35 40 45
 Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
 50 55 60
 Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| 65 | Lys | Cys | Thr | Pro | Lys | Met | Lys | Lys | Phe | Ile | Pro | Gly | Arg | Cys | His | Thr | 80 |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| Tyr | Glu | Gly | Asp | Lys | Glu | Ser | Ala | Gln | Gly | Gly | Ile | Gly | Glu | Ala | Ile | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | |
| Val | Asp | Ile | Pro | Glu | Ile | Pro | Gly | Phe | Lys | Asp | Leu | Glu | Pro | Met | Glu | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Gln | Phe | Ile | Ala | Gln | Val | Asp | Leu | Cys | Val | Asp | Cys | Thr | Thr | Gly | Cys | | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| Leu | Lys | Gly | Leu | Ala | Asn | Val | Gln | Cys | Ser | Asp | Leu | Leu | Lys | Lys | Trp | | |
| | | 145 | | | 150 | | | | | 155 | | | | | 160 | | |
| Leu | Pro | Gln | Arg | Cys | Ala | Thr | Phe | Ala | Ser | Lys | Ile | Gln | Gly | Gln | Val | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| Asp | Lys | Ile | Lys | Gly | Ala | Gly | Gly | Asp | | | | | | | | | |
| | | | 180 | | | | | 185 | | | | | | | | | |

<210> 21
 <211> 1146
 <212> DNA
 <213> Gaussia

<220>
 <221> CDS
 <222> (1)...(1146)
 <223> Nucleotide sequence encoding a CBD-Gaussia
 luciferase fusion protein

| | |
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| <400> 21 | |
| atg tca gtt gaa ttt tac aac tct aac aaa tca gca caa aca aac tca | 48 |
| Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser | |
| 1 5 10 15 | |
| att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat | 96 |
| Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn | |
| 20 25 30 | |
| tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa | 144 |
| Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln | |
| 35 40 45 | |
| gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc | 192 |
| Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser | |
| 50 55 60 | |
| tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca | 240 |
| Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr | |
| 65 70 75 80 | |
| gca agc cca aca tca acc tat gat aca tat gtt gaa ttt gga ttt gca | 288 |
| Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala | |
| 85 90 95 | |
| agc gga gca gct act ctt aaa aaa gga caa ttt ata act att caa gga | 336 |
| Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly | |
| 100 105 110 | |
| aga ata aca aaa tca gac tgg tca aac tac act caa aca aat gac tat | 384 |
| Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr | |
| 115 120 125 | |
| tca ttt gat gca agt agt tca aca cca gtt gta aat cca aaa gtt aca | 432 |
| Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr | |
| 130 135 140 | |
| gga tat ata ggt gga gct aaa gtt ctt ggt aca gca cca ggt tcc gcg | 480 |

| | | | | | | | | | | | | | | | | |
|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| Gly 145 | Tyr | Ile | Gly | Gly | Ala 150 | Lys | Val | Leu | Gly | Thr 155 | Ala | Pro | Gly | Ser | Ala 160 | |
| ggt | ctg | gtg | cca | cgc | ggt | agt | act | gca | att | ggt | atg | aaa | gaa | acc | gct | 528 |
| Gly | Leu | Val | Pro | Arg 165 | Gly | Ser | Thr | Ala | Ile 170 | Gly | Met | Lys | Glu | Thr 175 | Ala | |
| gct | gct | aaa | ttc | gaa | cgc | cag | cac | atg | gac | agc | cca | gat | ctg | ggt | acc | 576 |
| Ala | Ala | Lys | Phe 180 | Glu | Arg | Gln | His | Met 185 | Asp | Ser | Pro | Asp | Leu 190 | Gly | Thr | |
| gat | gac | gac | gac | aag | atg | gga | gtg | aaa | ggt | ctt | ttt | gcc | ctt | att | tgt | 624 |
| Asp | Asp | Asp | Asp 195 | Lys | Met | Gly | Val 200 | Lys | Val | Leu | Phe | Ala 205 | Leu | Ile | Cys | |
| att | gct | gtg | gcc | gag | gcc | aaa | cca | act | gaa | aac | aat | gaa | gat | ttc | aac | 672 |
| Ile | Ala | Val | Ala | Glu | Ala | Lys 215 | Pro | Thr | Glu | Asn | Asn 220 | Glu | Asp | Phe | Asn | |
| att | gta | gct | gta | gct | agc | aac | ttt | gct | aca | acg | gat | ctc | gat | gct | gac | 720 |
| Ile | Val | Ala | Val | Ala | Ser 230 | Asn | Phe | Ala | Thr | Thr 235 | Asp | Leu | Asp | Ala | Asp 240 | |
| cgt | ggt | aaa | ttg | ccc | gga | aaa | aaa | tta | cca | ctt | gag | gta | ctc | aaa | gaa | 768 |
| Arg | Gly | Lys | Leu | Pro 245 | Gly | Lys | Lys | Leu | Pro 250 | Leu | Glu | Val | Leu | Lys 255 | Glu | |
| atg | gaa | gcc | aat | gct | agg | aaa | gct | ggc | tgc | act | agg | gga | tgt | ctg | ata | 816 |
| Met | Glu | Ala | Asn 260 | Ala | Arg | Lys | Ala | Gly 265 | Cys | Thr | Arg | Gly | Cys 270 | Leu | Ile | |
| tgc | ctg | tca | cac | atc | aag | tgt | aca | ccc | aaa | atg | aag | aag | ttt | atc | cca | 864 |
| Cys | Leu | Ser 275 | His | Ile | Lys | Cys | Thr 280 | Pro | Lys | Met | Lys | Lys 285 | Phe | Ile | Pro | |
| gga | aga | tgc | cac | acc | tat | gaa | gga | gac | aaa | gaa | agt | gca | cag | gga | gga | 912 |
| Gly | Arg | Cys | His | Thr | Tyr | Glu 295 | Gly | Asp | Lys | Glu | Ser 300 | Ala | Gln | Gly | Gly | |
| ata | gga | gag | gct | att | gtt | gac | att | cct | gaa | att | cct | ggg | ttt | aag | gat | 960 |
| Ile | Gly | Glu | Ala | Ile | Val 310 | Asp | Ile | Pro | Glu | Ile 315 | Pro | Gly | Phe | Lys | Asp 320 | |
| ttg | gaa | ccc | atg | gaa | caa | ttc | att | gca | caa | gtt | gac | cta | tgt | gta | gac | 1008 |
| Leu | Glu | Pro | Met | Glu 325 | Gln | Phe | Ile | Ala | Gln 330 | Val | Asp | Leu | Cys | Val 335 | Asp | |
| tgc | aca | act | gga | tgc | ctc | aaa | ggt | ctt | gcc | aat | gtg | caa | tgt | tct | gat | 1056 |
| Cys | Thr | Thr | Gly 340 | Cys | Leu | Lys | Gly | Leu 345 | Ala | Asn | Val | Gln | Cys 350 | Ser | Asp | |
| tta | ctc | aag | aaa | tgg | ctg | cca | caa | aga | tgt | gca | act | ttt | gct | agc | aaa | 1104 |
| Leu | Leu | Lys 355 | Lys | Trp | Leu | Pro | Gln 360 | Arg | Cys | Ala | Thr | Phe 365 | Ala | Ser | Lys | |
| att | caa | ggc | caa | gtg | gac | aaa | ata | aag | ggt | gcc | ggt | ggt | gat | | | 1146 |
| Ile | Gln | Gly | Gln | Val | Asp 370 | Lys 375 | Ile | Lys | Gly | Ala | Gly 380 | Gly | Asp | | | |

<210> 22
 <211> 382
 <212> PRT
 <213> Gaussia

<400> 22

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Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
 1      5      10      15
Ile Thr Pro Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
 20      25      30
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
 35      40      45
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
 50      55      60
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
 65      70      75      80
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
 85      90      95
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
100     105     110
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
115     120     125
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
130     135     140
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145     150     155     160
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
165     170     175
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
180     185     190
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
195     200     205
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
210     215     220
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225     230     235     240
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
245     250     255
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
260     265     270
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
275     280     285
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
290     295     300
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305     310     315     320
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
325     330     335
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
340     345     350
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
355     360     365
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
370     375     380

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<210> 23

<211> 864

<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

<222> (61)...(762)

<223> GFP Clone-1

<400> 23

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atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc    108
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1      5      10      15

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aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt 156
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
      20      25      30

ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta 204
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
      35      40      45

aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct 252
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
      50      55      60

ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc 300
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
      65      70      75

gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac 348
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
      85      90      95

att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc 396
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
      100      105      110

ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat 444
Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
      115      120      125

cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag 492
Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
      130      135      140

cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa 540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
      145      150      155      160

tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac 588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
      165      170      175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg 636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
      180      185      190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc 684
Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
      195      200      205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca 732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
      210      215      220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc 782
Ile Lys Lys Ile Glu Gly Ser Leu Pro *
      225      230

tatgcacgta gcattttttt ggaaatataa gtgggtattgt tcaataaaaat attaaatata 842
aaaaaaaaaa aaaaaaaaaa aa
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<210> 24
<211> 860
<212> DNA
<213> Renilla reniformis

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<220>

<221> CDS

<222> (57)...(758)

<223> GFP Clone-2

<400> 24

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ggcacgaggc tgacacaata aaaaaccttt caaattgttt ctctgtagca ggaagt atg      59
                                     Met
                                     1

gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc aac      107
Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile Asn
                    5                      10                      15

tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt ggc      155
Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val Gly
                    20                      25                      30

gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta aca      203
Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val Thr
                    35                      40                      45

aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtt gct ttc      251
Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala Phe
                    50                      55                      60                      65

tca tat ggg aac aga gct tat act ggt tac cca gaa gaa att tcc gac      299
Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser Asp
                    70                      75                      80

tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac att      347
Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn Ile
                    85                      90                      95

cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc ttg      395
Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser Leu
                    100                      105                      110

gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat cta      443
Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp Leu
                    115                      120                      125

cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag cca      491
Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln Pro
                    130                      135                      140                      145

tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa tgt      539
Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu Cys
                    150                      155                      160

ata ata gca ttc aaa ctt caa act ggc aaa cat ttc act tac cac atg      587
Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His Met
                    165                      170                      175

agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg tat      635
Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu Tyr
                    180                      185                      190

cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc agt      683
His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala Ser
                    195                      200                      205

ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca atc      731
Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr Ile
                    210                      215                      220                      225

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aaa aaa att gaa ggc tct tta cca tag atatctatac acaattattc 778
 Lys Lys Ile Glu Gly Ser Leu Pro *
 230

tatgcacgta gcattttttt ggaaatataa gtgggtattgt tcaataaaat attaaatata 838
 aaaaaaaaaa aaaaaaaaaa aa 860

<210> 25
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 <212> DNA
 <213> Renilla reniformis

<220>
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 <222> (61)...(762)
 <223> GFP Clone-3

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 atg gat ctc gca aaa ctt ggt ttg aag gaa gtg atg cct act aaa atc 108
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1 5 10 15
 aac tta gaa gga ctg gtt ggc gac cac gct ttc tca atg gaa gga gtt 156
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
 20 25 30
 ggc gaa ggc aac ata ttg gaa gga act caa gag gtg aag ata tcg gta 204
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
 35 40 45
 aca aaa ggc gca cca ctc cca ttc gca ttt gat atc gta tct gtg gct 252
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
 50 55 60
 ttt tca tat ggg aac aga gct tat acc ggt tac cca gaa gaa att tcc 300
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
 65 70 75 80
 gac tac ttc ctc cag tcg ttt cca gaa ggc ttt act tac gag aga aac 348
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
 85 90 95
 att cgt tat caa gat gga gga act gca att gtt aaa tct gat ata agc 396
 Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
 100 105 110
 ttg gaa gat ggt aaa ttc ata gtg aat gta gac ttc aaa gcg aag gat 444
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
 115 120 125
 cta cgt cgc atg gga cca gtc atg cag caa gac atc gtg ggt atg cag 492
 Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
 130 135 140
 cca tcg tat gag tca atg tac acc aat gtc act tca gtt ata ggg gaa 540
 Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
 145 150 155 160
 tgt ata ata gca ttc aaa ctt caa act ggc aag cat ttc act tac cac 588
 Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
 165 170 175

atg agg aca gtt tac aaa tca aag aag cca gtg gaa act atg cca ttg 636
 Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
 180 185 190

tat cat ttc atc cag cat cgc ctc gtt aag acc aat gtg gac aca gcc 684
 Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
 195 200 205

agt ggt tac gtt gtg caa cac gag aca gca att gca gcg cat tct aca 732
 Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
 210 215 220

atc aaa aaa att gaa ggc tct tta cca tag atacctgtac acaattattc 782
 Ile Lys Lys Ile Glu Gly Ser Leu Pro *
 225 230

tatgcacgta gcattttttt ggaaatataa gtgggtattgt tcaataaaaat attaaatata 842
 tgcttttgca aaaaaaaaaa aaaaaaaaaa a 873

<210> 26
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 <212> DNA
 <213> Renilla reniformis

<220>
 <221> CDS
 <222> (61)...(759)
 <223> Human codon optimized Renilla reniformis GFP

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 atg gac ctg gcc aag ctg ggc ctg aag gag gtg atg ccc acc aag atc 108
 Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
 1 5 10 15

aac ctg gag ggc ctg gtg ggc gac cac gcc ttc tcg atg gag ggc gtg 156
 Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
 20 25 30

ggc gag ggc aac atc ttg gag ggc acc cag gag gtg aag atc agc gtg 204
 Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
 35 40 45

acc aag ggc gcc ccc ctg ccc ttc gcc ttc gac atc gtg agc gtg gcc 252
 Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
 50 55 60

ttc agc tac ggc aac cgg gcc tac acc ggc tac ccc gag gag atc agc 300
 Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
 65 70 75 80

gac tac ttc ctg cag agc ttc ccc gag ggc ttc acc tac gag cgg aac 348
 Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
 85 90 95

atc cgg tac cag gac ggc ggc acc gcc atc gtg aag agc gac atc agc 396
 Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
 100 105 110

ctg gag gac ggc aag ttc atc gtg aac gtg gac ttc aag gcc aag gac 444
 Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
 115 120 125

ctg cgg cgg atg ggc ccc gtg atg cag cag gac atc gtg ggc atg cag 492

Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
130 135 140

ccc agc tac gag agc atg tac acc aac gtg acc agc gtg atc ggc gag 540
Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145 150 155 160

tgc atc atc gcc ttc aag ctg cag acc ggc aag cac ttc acc tac cac 588
Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
165 170 175

atg cgg acc gtg tac aag agc aag aag ccc gtg gag acc atg ccc ctg 636
Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
180 185 190

tac cac ttc atc cag cac cgg ctg gtg aag acc aac gtg gac acc gcc 684
Tyr His Phe Ile Gln His Arg Val Lys Thr Asn Val Asp Thr Ala
195 200 205

agc ggc tac gtg gtg cag cac gag aca gcc atc gcc gcc cac agc acc 732
Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
210 215 220

atc aag aag atc gag ggc agc ctg ccc tagatacctg tacacaatta 779
Ile Lys Lys Ile Glu Gly Ser Leu Pro
225 230

ttctatgcac gtagcatttt ttgggaaata taagtgggtat tgttcaataa aatattaaat 839
ataaaaaaaaaa aaaaaaaaaa aaaaa 864

<210> 27

<211> 233

<212> PRT

<213> Renilla reniformis

<400> 27

Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1 5 10 15

Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
20 25 30

Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
35 40 45

Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
50 55 60

Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65 70 75 80

Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
85 90 95

Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Lys Ser Asp Ile Ser
100 105 110

Leu Glu Asp Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Lys Asp
115 120 125

Leu Arg Arg Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln
130 135 140

Pro Ser Tyr Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu
145 150 155 160

Cys Ile Ile Ala Phe Lys Leu Gln Thr Gly Lys His Phe Thr Tyr His
165 170 175

Met Arg Thr Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu
180 185 190

Tyr His Phe Ile Gln His Arg Leu Val Lys Thr Asn Val Asp Thr Ala
195 200 205

Ser Gly Tyr Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr
210 215 220

Ile Lys Lys Ile Glu Gly Ser Leu Pro

225

230

<210> 28
 <211> 861
 <212> DNA
 <213> Pleuromamma

<220>
 <221> CDS
 <222> (148)...(741)
 <223> Pleuormamma luciferase

<400> 28
 cggcaccgaga ttttgtctgt ggtgattggg attgtctgtc tctcaggtca agcagaaagt 60
 tcgctgaaag gtgatttctg tagtgatgtt tccttctggg atgtgatcaa gtacaacact 120
 gagagtcgac aatgctgtga cacaaaa atg ctt aga aat tgc gct agg aag caa 174
 Met Leu Arg Asn Cys Ala Arg Lys Gln
 1 5

gag caa gtt tgc gcc gat gtg acc gag atg aaa tgc caa gca gtt gct 222
 Glu Gln Val Cys Ala Asp Val Thr Glu Met Lys Cys Gln Ala Val Ala 25
 10 15 20 25

tgg gcc gac tgt gga ccc aga ttt gat tcc act ggc agg aat aga tgc 270
 Trp Ala Asp Cys Gly Pro Arg Phe Asp Ser Thr Gly Arg Asn Arg Cys 40
 30 35 40

caa gtt caa tac aag gac tac gcg tac aag tcc tgc gtg gaa gtt gat 318
 Gln Val Gln Tyr Lys Asp Tyr Ala Tyr Lys Ser Cys Val Glu Val Asp 55
 45 50 55

tac act gta ccg cac agg aag caa gtt cca gag tgc aaa caa gtc act 366
 Tyr Thr Val Pro His Arg Lys Gln Val Pro Glu Cys Lys Gln Val Thr 70
 60 65 70

aaa gat aac tgc gtt act gat tgg gaa gtt gac gcc aat ggc aac aag 414
 Lys Asp Asn Cys Val Thr Asp Trp Glu Val Asp Ala Asn Gly Asn Lys 85
 75 80 85

gtt tgg ggt ggt acc gag aaa tgc act cct gtc act tgg gaa gaa tgt 462
 Val Trp Gly Gly Thr Glu Lys Cys Thr Pro Val Thr Trp Glu Glu Cys 105
 90 95 100 105

aat atc gtg gag aaa gat gta gat ttt cca act gtc aag acg gaa tgc 510
 Asn Ile Val Glu Lys Asp Val Asp Phe Pro Thr Val Lys Thr Glu Cys 120
 110 115 120

ggc atc ctg tct cac ctt aag tat gca gac ttc ata gag gga cct tcc 558
 Gly Ile Leu Ser His Leu Lys Tyr Ala Asp Phe Ile Glu Gly Pro Ser 135
 125 130 135

cac tct ttg tct atg aga acc aat tgt cag gtc aag agt tca ttg gac 606
 His Ser Leu Ser Met Arg Thr Asn Cys Gln Val Lys Ser Ser Leu Asp 150
 140 145 150

tgc cgg cct gtt aag acc agg aag tgt gca acg gtc gag tac cac gaa 654
 Cys Arg Pro Val Lys Thr Arg Lys Cys Ala Thr Val Glu Tyr His Glu 165
 155 160 165

tgc agc atg aag ccc caa gaa gac tgc agc cca gtc act gtt cat att 702
 Cys Ser Met Lys Pro Gln Glu Asp Cys Ser Pro Val Thr Val His Ile 185
 170 175 180 185

cct gac cag gag aaa gtt cac cag aag aag tgc ctc aca taaatgttat 751

Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr
 190 195

caatttttagc tcttactaat ttaaacataa taaatatcac atcgaagccc tttattttat 811
 agaagtgtaa tgcttgaata aatctagtga ataaaaaaaa aaaaaaaaaa 861

<210> 29
 <211> 198
 <212> PRT
 <213> Pleuromamma

<400> 29
 Met Leu Arg Asn Cys Ala Arg Lys Gln Glu Gln Val Cys Ala Asp Val
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 Thr Glu Met Lys Cys Gln Ala Val Ala Trp Ala Asp Cys Gly Pro Arg
 20 25 30
 Phe Asp Ser Thr Gly Arg Asn Arg Cys Gln Val Gln Tyr Lys Asp Tyr
 35 40 45
 Ala Tyr Lys Ser Cys Val Glu Val Asp Tyr Thr Val Pro His Arg Lys
 50 55 60
 Gln Val Pro Glu Cys Lys Gln Val Thr Lys Asp Asn Cys Val Thr Asp
 65 70 75 80
 Trp Glu Val Asp Ala Asn Gly Asn Lys Val Trp Gly Gly Thr Glu Lys
 85 90 95
 Cys Thr Pro Val Thr Trp Glu Glu Cys Asn Ile Val Glu Lys Asp Val
 100 105 110
 Asp Phe Pro Thr Val Lys Thr Glu Cys Gly Ile Leu Ser His Leu Lys
 115 120 125
 Tyr Ala Asp Phe Ile Glu Gly Pro Ser His Ser Leu Ser Met Arg Thr
 130 135 140
 Asn Cys Gln Val Lys Ser Ser Leu Asp Cys Arg Pro Val Lys Thr Arg
 145 150 155 160
 Lys Cys Ala Thr Val Glu Tyr His Glu Cys Ser Met Lys Pro Gln Glu
 165 170 175
 Asp Cys Ser Pro Val Thr Val His Ile Pro Asp Gln Glu Lys Val His
 180 185 190
 Gln Lys Lys Cys Leu Thr
 195

<210> 30
 <211> 1104
 <212> DNA
 <213> Ptilosarcus gurneyi

<220>
 <221> CDS
 <222> (34)...(747)
 <223> Ptilosarcus Green Fluorescent Protein

<400> 30
 tcggcaccgag ctggcctcca cacttttagac aaa atg aac cgc aac gta tta aag 54
 Met Asn Arg Asn Val Leu Lys
 1 5
 aac act gga ctg aaa gag att atg tcg gca aaa gct agc gtt gaa gga 102
 Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly
 10 15 20
 atc gtg aac aat cac gtt ttt tcc atg gaa gga ttt gga aaa ggc aat 150
 Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn
 25 30 35
 gta tta ttt gga aac caa ttg atg caa atc cgg gtt aca aag gga ggt 198
 Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly
 40 45 50 55

ccg ttg cca ttc gct ttc gat att gtt tcc ata gct ttc caa tac ggg 246
 Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly
 60 65 70
 aat cgc act ttc acg aaa tac cca gac gac att gcg gac tac ttt gtt 294
 Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val
 75 80 85
 caa tca ttc ccg gct gga ttt ttc tac gaa aga aat cta cgc ttt gaa 342
 Gln Ser Phe Pro Ala Gly Phe Phe Tyr Glu Arg Asn Leu Arg Phe Glu
 90 95 100
 gat ggc gcc att gtt gac att cgt tca gat ata agt tta gaa gat gat 390
 Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp
 105 110 115
 aag ttc cac tac aaa gtg gag tat aga ggc aac ggt ttc cct agt aac 438
 Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn
 120 125 130 135
 gga ccc gtg atg caa aaa gcc atc ctc ggc atg gag cca tcg ttt gag 486
 Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu
 140 145 150
 gtg gtc tac atg aac agc ggc gtt ctg gtg ggc gaa gta gat ctc gtt 534
 Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val
 155 160 165
 tac aaa ctc gag tca ggg aac tat tac tcg tgc cac atg aaa acg ttt 582
 Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe
 170 175 180
 tac aga tcc aaa ggt gga gtg aaa gaa ttc ccg gaa tat cac ttt atc 630
 Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile
 185 190 195
 cat cat cgt ctg gag aaa acc tac gtg gaa gaa gga agc ttc gtg gaa 678
 His His Arg Leu Glu Lys Thr Tyr Val Glu Glu Gly Ser Phe Val Glu
 200 205 210 215
 caa cac gag acg gcc att gca caa ctg acc aca att gga aaa cct ctg 726
 Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu
 220 225 230
 ggc tcc ctt cat gaa tgg gtg tagaaaaatga ccaatatact ggggaaaccg 777
 Gly Ser Leu His Glu Trp Val
 235
 ataaccgttt ggaagcttgt gtatacaaat tatttggggt cattttgttaa tgtgtatgtg 837
 tgttgtatga tcaatagacg tcgtcattca tagcttgaat ccttcagcaa aagaaacctc 897
 gaagcatatt gaaacctcga agcatattga aacctcgacg gagagcgtaa agagaccgca 957
 caaattaacg cgtttcaacc agcagttgga atctttaaac cgatcaaaac tattaatata 1017
 aatatatata ccctgtataa cttatatata tctatatagt ttgatattga ttaaattctgt 1077
 tcttgatcaa aaaaaaaaaa aaaaaaa 1104

<210> 31
 <211> 1279
 <212> DNA
 <213> Ptilosarcus gurneyi

<220>
 <221> CDS
 <222> (7) ... (720)

<223> Ptilosarcus Green Fluorescent Protein (GFP)

<400> 31

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|---|-----|
| gacaaa atg aac cgc aac gta tta aag aac act gga ctg aaa gag att | 48 |
| Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile | |
| 1 5 10 | |
| atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt | 96 |
| Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe | |
| 15 20 25 30 | |
| tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg | 144 |
| Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu | |
| 35 40 45 | |
| atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac | 192 |
| Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp | |
| 50 55 60 | |
| att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac | 240 |
| Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr | |
| 65 70 75 | |
| cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt | 288 |
| Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe | |
| 80 85 90 | |
| ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att | 336 |
| Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile | |
| 95 100 105 110 | |
| cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag | 384 |
| Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu | |
| 115 120 125 | |
| tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc | 432 |
| Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala | |
| 130 135 140 | |
| atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc | 480 |
| Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly | |
| 145 150 155 | |
| gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac | 528 |
| Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn | |
| 160 165 170 | |
| tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg | 576 |
| Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val | |
| 175 180 185 190 | |
| aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc | 624 |
| Lys Glu Phe Pro Glu Tyr His Phe Ile His Arg Leu Glu Lys Thr | |
| 195 200 205 | |
| tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca | 672 |
| Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala | |
| 210 215 220 | |
| caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg | 720 |
| Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val | |
| 225 230 235 | |
| tagaaaaatga ccaatataact ggggaaaaatc accaatatac tggggaaaaat gaccaattta | 780 |
| ctggggaaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat | 840 |

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ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca 900
aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt 960
gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga 1020
cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc 1080
gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt 1140
aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata 1200
tctacatagt ttgatattga ttaaactctgt tcttgatcac taaaaaaaaa aaaaaaaaaa 1260
aaaaaaaaaa aaaaaaaaaa 1279

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<210> 32
<211> 238
<212> PRT
<213> Ptilosarcus gurneyi

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<400> 32
Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
1 5 10 15
Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
20 25 30
Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
35 40 45
Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60
Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65 70 75 80
Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
85 90 95
Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110
Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125
Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
130 135 140
Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145 150 155 160
Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
165 170 175
Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
180 185 190
Phe Pro Glu Tyr His Phe Ile His Arg Leu Glu Lys Thr Tyr Val
195 200 205
Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
210 215 220
Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225 230 235

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<210> 33
<211> 233
<212> PRT
<213> Renilla Reniformis mutein

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<400> 33
Met Asp Leu Ala Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys Ile
1 5 10 15
Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly Val
20 25 30
Gly Glu Gly Asn Ile Leu Glu Gly Thr Gln Glu Val Lys Ile Ser Val
35 40 45
Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Val Ala
50 55 60
Phe Ser Tyr Gly Asn Arg Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser
65 70 75 80
Asp Tyr Phe Leu Gln Ser Phe Pro Glu Gly Phe Thr Tyr Glu Arg Asn
85 90 95
Ile Arg Tyr Gln Asp Gly Gly Thr Ala Ile Val Asp Ser Asp Ile Ser

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| | | | | | |
|-------------|---|--|-----|--|-----|
| | 100 | | 105 | | 110 |
| Leu Glu Asp | Gly Lys Phe Ile Val Asn Val Asp Phe Lys Ala Asp Asp | | | | |
| | 115 | | 120 | | 125 |
| Leu Arg Asp | Met Gly Pro Val Met Gln Gln Asp Ile Val Gly Met Gln | | | | |
| | 130 | | 135 | | 140 |
| Pro Ser Tyr | Glu Ser Met Tyr Thr Asn Val Thr Ser Val Ile Gly Glu | | | | |
| | 145 | | 150 | | 155 |
| Cys Ile Ile | Ala Phe Lys Leu Gln Thr Gly Lys Asp Phe Thr Tyr His | | | | |
| | 165 | | 170 | | 175 |
| Met Arg Thr | Val Tyr Lys Ser Lys Lys Pro Val Glu Thr Met Pro Leu | | | | |
| | 180 | | 185 | | 190 |
| Tyr His Phe | Ile Gln His Asp Leu Val Lys Thr Asn Val Asp Thr Ala | | | | |
| | 195 | | 200 | | 205 |
| Ser Gly Tyr | Val Val Gln His Glu Thr Ala Ile Ala Ala His Ser Thr | | | | |
| | 210 | | 215 | | 220 |
| Ile Asp | Lys Ile Glu Gly Ser Leu Pro | | | | |
| | 225 | | 230 | | |